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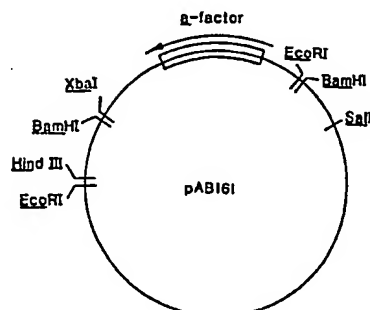
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(64) **A-factor and its processing signals.**

(57) Novel DNA constructs are provided for efficient expression of polypeptides by yeasts. The constructs employ yeast *a*-factor secretion leader and processing signals joined to a DNA sequence encoding a polypeptide of interest in reading frame with the *a*-factor signals. The constructions provide for the expression, secretion and maturation of the desired polypeptide. A strategy is provided for the isolation of the *a*-factor secretion leader and processing signals and the joining, by means of a relatively short adaptor, molecules of the DNA sequence encoding the polypeptide to the processing signals in proper reading frame.

The bacterial cell strain *E. coli* HB101 (pAB163) was deposited at the A.T.C.C. on April 20, 1983 and given Accession No. 39342.



**FIG. 1**

9729-2

a-FACTOR AND ITS PROCESSING SIGNALSBACKGROUND OF THE INVENTIONField of the Invention

5           The initial stages of the biological  
revolution demonstrated the feasibility of obtaining  
expression of mammalian genes in lower organisms.  
Because of the much greater amount of knowledge associ-  
10   ated with the regulatory sequences of bacteria, bacteria  
were chosen as the initial host for producing hetero-  
ologous proteins. However, bacteria have many  
shortcomings. Not least of these shortcomings is the  
fact that they produce an enterotoxin which must be  
15   completely removed, if the product is to be  
administered to a mammalian recipient, e.g. as a  
pharmaceutical agent.

          Furthermore, the codons of the heterologous  
genes will be expressed with relatively low efficiency,  
20   since the preferred codons of the source of the hetero-  
ologous protein and the host will be substantially  
different. In addition, where the product of interest  
needs to be processed, such as glycosylated, matured by  
removal of polypeptide sequences, or assembled, bacteria  
25   frequently prove to be incapable or inefficient at  
these processes. Moreover, for commercial application  
of genetic engineering technology it would be desirable  
for ease of subsequent purification if synthesized  
products were secreted into the growth medium, a  
30   process in bacteria of only limited, laboratory scale  
use. It is therefore desirable to find alternative  
hosts.

          Yeast as a host has many advantages which  
recommend its use. The commercial fermentation of  
35   yeast is well established. Yeast is a eukaryote unlike  
bacteria, so that it shares greater similarities with  
mammalian organisms. Yeasts are thus capable of many  
of the processing steps observed in higher organisms

and secretion of several natural polypeptides and proteins is known. Furthermore, yeasts do not produce enterotoxins.

It is therefore desirable to provide yeast  
5 regulatory signals which may be employed for the efficient production of heterologous proteins in yeast. While the existence of the regulatory signals may be predicted, their isolation, manipulation, and ultimately establishing that the regulatory signals can operate  
10 with alien flanking regions in conjunction with a foreign DNA sequence is long and arduous work, requiring well thought out experimental design, careful manipulation, and rigorous proofs of having achieved the intended result at each of the many stages involved.

15 Description of the Prior Art

Betz and Duntze, Eur. J. Biochem. (1979) 95:469 report the initial isolation and preliminary characterization of mature  $\alpha$ -factor peptide and Betz, Manney and Duntze, Gamete Res. (1981) 4:571-584 propose  
20 an amino acid sequence for the mature  $\alpha$ -factor peptide. Kurjan and Herskowitz, Cell (1982) 30:933-943 describe a putative  $\alpha$ -factor precursor, describe the sequence and postulate a processing mechanism. U.S. Patent Nos. 4,336,326 and 4,338,397 describe sequences encoding for  
25 leaders in prokaryotes. Julius et al., Cell (1983) 32:839-852 describe the role of a membrane dipeptidase in the processing of  $\alpha$ -factor. See also copending application Serial No. 457,325, filed January 12, 1983, which is incorporated herein by reference, where such  
30 application describes the use of the  $\alpha$ -factor leader and processing signals for expression of a heterologous polypeptide.

SUMMARY OF THE INVENTION

Yeast  $\alpha$ -factor in combination with its  
35 regulatory signals is detected, isolated, and manipulated to provide for joining to a DNA sequence encoding a polypeptide of interest. The resulting construct

provides for expression and maturation of the polypeptide with secretion of the polypeptide into the nutrient medium. An experimental design is provided for the manipulation of the yeast a-factor gene to provide for joining of a DNA coding sequence by means of small adaptor molecules to the yeast a-factor leader and processing signals in proper reading frame.

DESCRIPTION OF THE FIGURE

Figure 1 is a diagram of the plasmid pAB161.

10 DETAILED DESCRIPTION OF SPECIFIC EMBODIMENTS

In accordance with the subject invention, eukaryotic hosts, particularly yeasts, are employed for the production of secreted, usually mature or maturable, polypeptides, where such polypeptides may be harvested from a nutrient medium. The polypeptides are produced by employing a DNA construct encoding for yeast a-factor secretion leader and processing signals joined in proper reading frame to a DNA sequence encoding for a polypeptide of interest. The resulting construct encodes for a pro-polypeptide, which will contain the signals for secretion of the pro-polypeptide and processing of the polypeptide, either intra- or extracellularly, desirably to the mature polypeptide. Where the pro-polypeptide is incompletely processed, appropriate peptidases, particularly membrane peptidases, may be employed for completing the maturation of the pro-polypeptide. This invention contemplates the production of secreted pro-polypeptide, partially processed pro-polypeptide and mature polypeptide and mixtures thereof.

Constructs of the subject invention will have the following formula defining a pro-polypeptide:

((PS) - (a-factor))<sub>n</sub> - PS - gene

35

wherein:

PS indicates yeast-recognizable processing signals for cleavage and removal of amino acids, the processing signals including at least two basic amino acids, which basic amino acids are lysine and arginine;

5           a-factor intends the DNA sequence encoding for at least a portion of the mature a-factor, usually the entire a-factor;

n is 0 or 1; and

"gene" intends a DNA sequence other than  
10 a-factor having an open reading frame encoding for a polypeptide of interest, which is joined at the terminal base of the immediately preceding PS (the processing signal) in proper reading frame. For the purposes of this invention "gene" encompasses fused proteins, where  
15 a structural gene may be inserted into another structural gene in proper reading frame, portions or complete structural genes joined together or arbitrary synthetic sequences having no known natural analog.

For the most part, the DNA constructs of the  
20 subject invention will have at least the following formula:

$$L - (PS - (\underline{a}\text{-factor}))_n - PS - \text{gene}$$

25 wherein:

L intends the yeast a-factor secretory leader sequence, or similar sequence providing for secretion; and

all the other symbols have been defined  
30 previously.

PS will for the most part have the following formula:

$$B - D - F - H$$

wherein:

35 B and D are the same or different, and define the codons for the basic amino acids lysine and arginine, preferably being AAG; and

F and H are the same or different and define the codons for the acidic amino acids, aspartic or glutamic acid or the amides thereof, asparagine or glutamine, preferably being a combination of acid and amide, more preferably, F being GAC and H being AAC. The preferred DNA sequence is the naturally occurring DNA sequence encoding for lys-lys-asp-asn.

Alternatively, PS may have the formula:

$$((B-D)_s - (F-H)_t - (B-D)_u)_v$$

wherein:

s and v are 1-3; and

t and u are 0-3.

Thus, the processing signal may be varied by elimination of the acid amino acids and their amides or increasing the number of basic amino acids or providing for multiple dipeptides or tetrapeptides having the acid amino acid and the amide of the acid amino acid as repetitive dipeptide sequences or having the two basic amino acids in addition. However, for the most part, these additional amino acids will add a further complication to the organization of the construct, and therefore normally will not be used.

The secretion leader sequence of yeast a-factor is relatively short, being about 15 to 20 amino acids, more particularly, about 17 amino acids. The leader sequence has a methionine at its N-terminus.

In order for the polypeptide of interest to be expressed, it will be necessary to prepare a construct which will have a competent replication system and transcriptional regulatory signals for use in yeast. However, to the extent that the secretion and processing signals will be recognized by hosts other than yeast, replication systems for such other hosts may be employed. Usually the construct will include other functional DNA sequences as well, where the

function may have been employed during the construction of the construct or may serve a useful function during the expression of the polypeptide.

Constructs can be prepared which are provided  
 5 with the necessary transcriptional regulatory signals. That is, such constructs will include a RNA polymerase binding site, which may have contiguous or non-contiguous sequences, which binding site may be the wild type for a-factor or may be the RNA polymerase  
 10 binding site for a variety of other yeast genes, such as the promoters concerned with enzymes involved in the glycolytic pathway, such as phosphoglucokinase, glyceraldehyde-3-phosphate dehydrogenase, pyruvate kinase, phosphoglucoisomerase, triosephosphate isomerase,  
 15 alcohol dehydrogenase, etc., or with metallothionein, viral promoters, or the like. Reference to these promoters may be found in Hitzeman et al., J. Biol. Chem. (1980) 255:12073-12080.

In addition to the promoters, various  
 20 sequences regulating the promoters may also be employed, such as enhancers and DNA binding sites for repressors, derepressors, activators, and the like. Other DNA sequences which may be involved include ribosomal binding sites, cap sequence, stop codons, transcrip-  
 25 tional terminator, etc. One or more of these sequences may be present as part of the construct or may be available as a part of a replication system which may serve as a vector. Usually, the replication system will be associated with other functions to be described  
 30 subsequently.

The yeast a-factor promoter and leader region may be joined to a yeast replication system, e.g. 2 $\mu$ m plasmid and/or ARS1 + CEN3 to provide an expression vector having one or more convenient restriction sites.  
 35 This expression vector may be formulated as follows:

$$P-L-(PS-(\underline{a}\text{-factor}))_n-(PS-(\text{gene})_r)_w-|RepS|_q;$$

or more particularly as follows:

$$\text{-RS-P-(cap)}_m\text{-(RBS)}_p\text{-ic-L'-(PS-(a-factor))}_n\text{-}$$

$$\text{PS-gene-sc-T-|RepS|}_q$$

5

wherein:

PS and gene have been defined previously;

RS intends regulatory signals which may be on  
either side of P and includes enhancers and DNA binding  
10 sites for repressors, derepressors and activators;

P is an RNA polymerase binding site or  
promoter, particularly the a-factor wild-type promoter;

cap is a capping sequence;

ic is the f-met initiation codon, which is  
15 part of the secretion leader sequence;

L' is a DNA sequence which with ic defines  
the amino acid sequence of the a-factor leader or  
similar sequence providing for secretion;

sc intends one or more stop codons;

20 T intends a transcriptional terminator;

|RepS| intends a replication system which may  
be at any position in the vector external to the  
immediate expression region of the construct, generally  
an episomal or viral replication system having other  
25 than the wild-type flanking regions;

m, n and p and r are 0 or 1;

q is at least 1 and may be 2 or more, usually  
1 to 2;

w is 0 or a small integer, generally 3 or  
30 less, with at least one of n or w being 1;

wherein the construct may be linear or  
circular and except for |RepS| the various sequences  
are in the order indicated with the promoter directed  
toward the gene.

35 The leader secretion sequence will for the  
most part encode for the following polypeptide sequence:



met-gln-pro-ser-thr-ala-thr-ala-ala-  
pro-lys-glu-lys-thr-ser-ser-glu

The processing signal sequence will for the  
5 most part encode for a polypeptide sequence of the  
following formula:

			asp	asp
	lys	lys	asn	asn
10	arg	arg	glu	glu
			gln	gln

where any amino acid in a column may be employed. Of  
particular interest is the DNA sequence (unless other-  
15 wise indicated, sequences will read in the 5'-3'  
direction):

AAG AAG GAC AAC

encoding for the natural processing signal having the  
following amino acid sequence:

20 lys lys asp asn.

The cloning and expression constructs will  
generally be from about 5 to 50kbp (kilobase pairs),  
where plasmids will generally range from about 5 to  
25kbp. Where viral vectors are used, packaging  
25 requirements may result in constructs of up to about  
50kbp.

One strategy for developing the constructs of  
this invention is as follows: The DNA sequence encoding  
for the pro-a-factor can be obtained from the yeast  
30 genome by any convenient means, e.g. detection by  
hybridization with labeled probes. Where the fragment  
is greater than about 1000bp, the fragment may be  
reduced by appropriate cleavage at available restriction  
sites. Conveniently, within the a-factor gene near the  
35 C-terminus of the mature peptide is an AvaII restriction  
site and the AvaII restricted fragment may be resected,  
so as to have the terminus of the fragment at a conve-  
nient site upstream from and proximal to the first base

of the a-factor coding sequence. Preferably, the terminus is in the processing signal sequence, more preferably 29 bases upstream from the AvaII cleavage site. This fragment may then be ligated to linkers  
5 having a flush end and a cohesive end, where the linker encodes, by itself or in combination with the terminal bases of the fragment, for an endonuclease recognition site. Particularly, if one resects 29 bases so that the three 3'-terminal bases of the fragment are 5'-AGG,  
10 by adding a linker having 5'-CCT, a StuI (5'-AGGCCT-3') site is created, so that one can screen for the desired fragment. In the illustrative example, after addition of the linker and any other appropriate manipulation, e.g. endonuclease digestion, plasmids may then be  
15 screened for the StuI site which was created by the linker containing the 5'-sequence CCT which was joined to the 3'-terminal AGG to define the StuI site. The plasmids may additionally be pre-screened, if desired, using a radiolabeled oligonucleotide probe complementary  
20 to the desired junction sequence.

A linker is employed which encodes a recognition site for an endonuclease which cleaves away from the recognition site. Furthermore, the asymmetry of the recognition site directs the cleavage upstream,  
25 generally about three to fifteen bases upstream from the recognition sequence. In the present example, the recognition site is a HgaI site. The presence of the StuI site ensures that the HgaI cleavage site is in the a-factor secretion leader sequence. With the HgaI  
30 cleavage in the a-factor leader region of the gene, the overhang DNA sequence is not a recognition sequence for an endonuclease which would be employed in further construction.

The a-factor leader fragment now contains  
35 both StuI and HgaI recognition and restriction sites either of which may be used for further manipulation.

By appropriate selection of restriction enzymes and adaptors, one can provide for linking the leader sequence to a gene through the processing signals, where the gene is in reading phase with the leader sequence, to provide a DNA fragment encoding for the pro-polypeptide. By providing for convenient restriction sites outside of the coding region for the joined leader and gene DNA sequence, one may clone the coding fragment for the pro-polypeptide and transcriptional regulatory signals, if present, in a cloning vehicle and then excise the coding fragment from the cloning vehicle and, as appropriate, insert the fragment into an expression vector in appropriate juxtaposition to the transcriptional regulatory signals. Preferably, and as will be described subsequently, one employs restriction sites, where the transcriptional regulatory signals of the a-factor are retained so that the construct which is inserted into the expression vector does not require the presence of a promoter, although tandem promoters are permissible.

The a-factor leader and processing signals and the strategy described above can be used for the expression of any polypeptide of interest, either derived from yeast or heterologous to yeast. For the most part, the polypeptides of interest will be naturally occurring polypeptides from other than yeast, particularly mammals, more particularly primates, and most frequently domestic animals or human. In addition, synthetic polypeptides may also be of interest.

The construct provides a portable sequence for insertion into vectors where the construct may be joined to include the gene of interest for expression. The resulting replication construct provides a convenient replication system with transcriptional signals as well as secretory and processing signals and having a restriction site which by the use of adaptors allows for insertion of a gene encoding a polypeptide of

interest in reading frame with the secretory and processing signals. Thus one can obtain expression of such gene in a host recognizing the yeast secretory signals to produce a secreted processed pro-polypeptide.

5           The final construct will be an episomal element capable of stable maintenance in a host, particularly a fungal host such as yeast. The construct includes one or more replication systems, desirably two replication systems, which individual replication  
10 systems may be a single sequence or non-contiguous plural sequences, allowing for both maintenance in the expression host, particularly yeast, and cloning in a prokaryote. In addition, one or more selection markers may be included, which will allow for selective pressure  
15 for maintenance of the episomal element in either or both of the hosts. Furthermore, the episomal element may be maintained at high or low copy number, the copy number generally ranging from about 1 to 200, more usually from about 1 to 100. With high copy number  
20 episomal elements, the number of copies will generally be at least 10, usually at least 20, and usually not exceeding about 150, more usually not exceeding about 100 copy number.

          Depending upon the particular polypeptide of  
25 interest, either high or low copy numbers may be desirable, taking into consideration the effect of the polypeptide product on the host and the efficiency of secretion. Where the presence of the expression product of the gene may have a deleterious effect on  
30 the viability of the host, a low copy number may be indicated.

          Various hosts, particularly yeast hosts, may be employed, particularly mutants having desired properties, either lesions allowing for complementation,  
35 mutants lacking or having specific regulatory systems, or the like. It should be appreciated that depending upon the rate of production of the expression product

of the construct, the processing enzyme may or may not be adequate for processing at that level of production. Therefore, a mutant having enhanced production of the processing enzyme(s) may be indicated or enhanced  
5 production of the enzyme(s) may be provided by means of an episomal element. Generally, the production of the enzyme should be of a lower order than the production of the desired expression product.

Alternatively, there may be situations where  
10 intracellular processing is not desired. In this situation, mutants would be desirable which lack the processing enzymes in their membrane or have relatively inefficient processing. In this situation, the product can be subsequently processed in vitro.

15 Furthermore, the structural gene may be present as a repeating unit in tandem, with intervening processing signals. The product may then be processed in whole or in part, with the result that one will obtain the various poly(amino acid) sequences either  
20 individually or in tandem for subsequent processing. In many situations, it may be desirable to provide for different tandem sequences, where each of the sequences is a subunit of a particular protein product. In some situations it may be desirable to eliminate the processing signals intervening between adjacent tandem  
25 heterologous structural genes so as to provide for the production of a multifunctional fusion product.

The structural gene may encode for any type of polypeptide of interest. The polypeptide may be as  
30 small as an oligopeptide of eight amino acids or may be 100,000 daltons or higher. Usually, single chains will be less than about 300,000 daltons, more usually less than about 150,000 daltons. Of particular interest are polypeptides of from about 5,000 to 150,000 daltons,  
35 more particularly of about 5,000 to 100,000 daltons. Illustrative polypeptides of interest include hormones and factors, such as growth hormone, somatomedins

epidermal growth factor, etc.; the endocrine secretions, such as luteinizing hormone, thyroid stimulating hormone, relaxin, secretin, oxytocin, insulin, vasopressin, renin, calcitonin, follicle stimulating hormone, prolactin, etc.; hematopoietic factors, e.g. erythropoietin, colony stimulating factor, etc.; lymphokines, e.g. interleukin-2; globins, globulins, e.g. immunoglobulins, albumins; interferons, such as  $\alpha$ ,  $\beta$  and  $\gamma$ ; regulatory proteins and repressors; enzymes and structural proteins; endorphins, e.g.  $\beta$ -endorphin, enkephalin, dynorphin, mammalian pathogen proteins, e.g. HBsAg, capsid proteins, etc.

Having prepared the episomal elements containing the constructs of this invention, one may then introduce such element into an appropriate host. The manner of introduction is conventional, there being a wide variety of ways to introduce DNA into a host. Conveniently, spheroplasts are prepared employing the procedure of, for example, Hinnen et al., PNAS USA (1978) 75:1919-1933 or Stinchcomb et al., EP 0 045 573. The transformants may then be grown in an appropriate nutrient medium and where appropriate, selective pressure maintained on the transformants. Where expression is inducible, one can allow for growth of the yeast to high density and then induce expression. In those situations where although secreted, a substantial proportion of the product may be retained in the periplasmic space, one can release the product by treating the yeast cells with an enzyme such as zymolase or lyticase.

The product may be harvested by any convenient means, e.g. centrifugation and the protein then purified by filtration, chromatography, electrophoresis, dialysis, solvent-solvent extraction, etc.

In accordance with the subject invention, one can provide for secretion of a wide variety of polypeptides, so as to greatly enhance product yield,

simplify purification, minimize degradation of the desired product, and simplify the processing equipment and engineering requirements. Furthermore, utilization of nutrients based on productivity can be greatly enhanced, so that more economical and more efficient production of polypeptides may be achieved. Also, the use of yeast has many advantages both in avoiding enterotoxins, which may be present with prokaryotes, and in employing known fermentation techniques, which have been developed for yeast over long periods of time, which techniques include isolation of yeast products.

The following examples are offered by way of illustration and not by way of limitation.

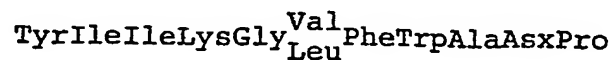
#### EXPERIMENTAL

##### Isolation of the a-factor Structural Gene

A collection of oligonucleotides with the following sequences is synthesized:



These oligonucleotides are used to probe by hybridization of a yeast DNA fragment library cloned in the plasmid YEp13 (Nasmyth and Tatchell, Cell (1980) 19:753). This oligonucleotide pool is designed to include molecules complementary to a region of DNA encoding the a-factor peptide, based on the reported structure of the mature a-factor peptide (Betz et al., op.cit., infra). The amino acid sequence of the mature a-factor peptide is reported as:



and the oligonucleotide probe extends from the first 5'-base encoding the second Ile through the second base of Asx.

A 19.5kb plasmid, pAB151, is identified by hybridization to this oligonucleotide pool. Following digestion of pAB151 with the restriction enzymes EcoRI and XbaI, a 1500bp fragment is identified which contains the hybridization detected segment of DNA. Following repair of the overhanging ends of this fragment with DNA polymerase Klenow fragment and the addition of BamHI oligonucleotide linkers, this fragment is ligated into the BamHI site of plasmid pBR322 to obtain plasmid pAB161, a 5900bp plasmid. Where the direction of the fragment is determined by the coding direction of the a-factor gene, upstream from the fragment is a SalI fragment, an EcoRI fragment at about the site of the BamHI site upstream from the a-factor and an EcoRI downstream from the downstream BamHI site and the HindIII site proximal to the downstream EcoRI site and intermediate the downstream EcoRI and BamHI sites (see Figure 1).

#### Structure of the Putative a-factor Structural Gene

The DNA sequence of the insert in pAB161 is determined and found to consist of 1569 base pairs. A region of this DNA is found to contain nucleotides coding for most of the reported a-factor peptide sequence. This sequence is part of a putative a-factor precursor coding sequence as shown in the sequence on the following page.



GAATTCGAGACTCAAAGATGCTGTACCGTTCACGCCGTTTAACGGTGATAGAGAAGCACACCCAAGGTTTACGTTGAAA  
GGTTCAGTATACAATGACCCATTCATCAAAGATCTTGAGCACAGGAAAGAATTTATTGCGTCTGGGTCAACACTAATT  
ATGCGTACGAAAGGGTGTGACAGAGGCATTTATGGGCTTAGGATGTGTTATATCCGAGGAGCTTTAAACATCAGGAT  
AGTGTGCAACGTGGCATAAGCTATGTAATCAACTACTTTTTATTTTCTATGTACGCATATACATGCATTACGATCTGT  
5 TTCAGTGTTCAGAAAAAAGGCACCTACTGCTACGGTTGGCCCATACCTTTATTCTTTGTTCTTGTACAAACGAGTGTG  
TAATTACCCAAAAAGGAAATTTACATGTTAAATGAAACCCAGTAATCAGAAAAACAGTTAAGAAACCTAAATGGTAG  
AGATAAAGATACAGATTCAGTGGTTGCTGAAAAATCAAGTAAAAAATGAAATAGAGTCTTCATATATAAACCGCCAGAA  
ATGAATTAATGAGAGGGATCTGTAAGTGTCTCGGATAAAACCAAATAAGTACAAAGCCATCGAATAGAA 1  
met  
ATG  
10 10 20  
gln pro ser thr ala thr ala ala pro lys glu lys thr ser ser glu lys lys asp asn  
CAA CCA TCT ACC GCT ACC GCC GCT CCA AAA GAA AAG ACC AGC AGT GAA AAG AAG GAC AAC  
30 36  
tyr ile ile lys gly val phe trp asp pro ala cys val ile ala AM  
15 TAT ATT ATC AAA GGT GTC TTC TGG GAC CCA GCA TGT GTT ATT GCT TAG TTTCTGCGTACAAAA  
ACGTTGTTCTCCCTCCTTTATCTTCCTTTTCCGCTACACCAATATATCATGTTTGTTCGTAATATTTCTTTTTAGACC  
TAATAATAAATATCCTAAGTAACTATATTATATAAAATATTTTGATACCTGTACCTGCTTTTGGTTATCGTTGTACA  
TCCATGCACACGCTCATATATATATATATATATATATATATATGTATATGTACATATAGCGCTTACCACCTACCGTGAAG  
TATATGTAAGGGTCTTCGCACCCGGATATCCCTTGTGGGATCTTGGATGCGGATGGTGAGTGTAACAGGCCTCATAA  
20 AGCTGTCTCTGTGTGCGGGAAGATGTCGTTTCATCGGCTTCGACCTCCTTATCTTGCTTCGATTGTTTCTTCGTA  
AGAGGGAGGATCTACGGGCAGCGGGTCTGCTCTCCTTGTATGCATGCTTATTTATATCACTCTTTCGCTATCCAT  
CATAATCTGTTTTTGTATGTGCTTTGAATACTCAACACATAAAATAATATCCAGTTAATTGTGCTGTGCCATTGA  
CGCTTTCCTTTGTCCCTTTAGACTGTCTTTATTGTGAAATATGCACGGCTGAGAATTACGTATACAGTGACTATCGT  
ATGGGGCGACAAAAGTTCCAGCGAGAAACAAGATGAAGCAGACTGGGGCCTGCCTGTATGGAGGGAAGCATAAGTTA  
25 ATATACCTCCAGATATTTGCAGATTAGGATACTGAACTGACGAAGACCTACGCTACACAACGAAGATAACACATGCTG  
GCACAAACATTCAAAAAACACACAGAGCCGTTCTAGA

Translated Mol. Weight = 3927.15

Biological evidence of two types is obtained that show that the 1500bp BamHI fragment in pAB161 contains a functional a-factor structural gene:

(1) The plasmid pAB161 is used to probe RNA from  
5 S. cerevisiae strains of a haploid, α haploid or a/α diploid mating type. Only cells of the a mating type produce RNA which hybridizes to pAB161. Therefore, the insert in pAB161 encodes an a-specific gene.

(2) The 1500bp BamHI fragment from pAB161 is  
10 ligated into the BamHI site of the high-copy yeast plasmid pC1/1 to obtain the plasmid pAB163. (Plasmid pC1/1 is a derivative of pJDB219 (Beggs, Nature (1978) 275:104) in which the region corresponding to bacterial plasmid pMB9 in pJDB219 has been replaced by pBR322 in  
15 pC1/1. pC1/1 contains a complete yeast 2μm replicator, yeast LEU2 gene and complete pBR322.)

pAB163 is introduced into the yeast strain AB101 (a leu2 ura3 his4 trp1) by transformation and selection of Leu<sup>+</sup> transformants. These transformants  
20 are found to produce at least ten-fold greater amounts of a-factor than does a control strain, as judged by a replica plating bioassay.

In comparison with the amino acid sequence reported by Betz et al. (op.cit., infra), the DNA  
25 sequence of pAB161 encodes additional amino acids both amino-terminal and carboxy-terminal to the mature a-factor sequence. Additionally, there is a difference in the order of amino acids corresponding to the carboxyl terminus of the mature a-factor peptide (DNA  
30 sequence yields: -TrpAspProAla-; reported peptide sequence: -TrpAlaAsxPro).

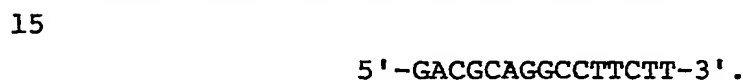
#### Preparation of Constructs

The following was the exemplary procedure for a construct employing human epidermal growth factor as  
35 the gene for expression. Plasmid pAB161 is cleaved with AvaII and the resulting fragments are resected

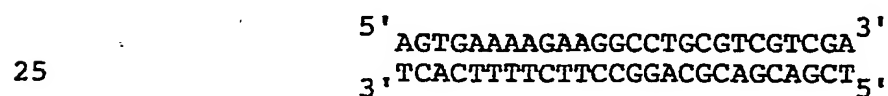
with nuclease Bal31 to remove approximately 29bp from each end. An oligonucleotide with the sequence



is ligated to the resulting mixture. The ligation mixture is digested with the enzymes BamHI and SalI and fragments of approximately 690bp are gel isolated.  
 10 These fragments are ligated to pBR322 which has been digested with BamHI and SalI. The resulting plasmids are screened for molecules hybridizing to a  $^{32}\text{P}$ -radiolabeled chemically synthesized oligonucleotide probe with the following sequence:



Plasmids so selected are then additionally screened for the presence of a StuI site. Such molecules are  
 20 created by the junction of the above oligonucleotide at the desired position of the a-factor gene as shown below:



The resulting molecule now has both a StuI and a HgaI recognition site adjacent to the region encoding the a-factor leader of the a-factor precursor.  
 30 Cleavage with StuI results in cleavage in the a-factor leader region of the gene, as shown below:



Alternatively, one may employ HgaI for a-factor leader cleavage to generate the product shown below:

5' AGTGAA 3'  
3' TCACTTTTCTT 5'

5 Either of these product sequences can then be joined to a DNA molecule containing the gene for human epidermal growth factor derived by cleavage of plasmid p328EGF-1.

The DNA sequence obtained from cleavage of p328EGF-1 with HgaI is as follows:

10 AACTCCGACTCCGAATGTCCATTGTCCCACGACGGTTACTGTTTGCACGACGGTGTTTGT  
GCTGAGGCTTACAGGTAACAGGGTGCTGCCAATGACAAAGCTGCTGCCACAAACA  
ATGTACATCGAAGCTTTGGACAAGTACGCTTGTAAGTGTGTTGGTTACATCGGTGAA  
TACATGTAGCTTCGAAACCTGTTTCATGCGAACATTGACACAACAACCAATGTAGCCACTT  
AGATGTCAATACAGAGACTTGAAGTGGTGGGAAT  
TCTACAGTTATGTCTCTGAACTTCACCACCCTTAAGTCT

15

Ligation of these molecules is carried out with the following oligonucleotide adaptor molecules:

Either

(1) a StuI-HgaI adaptor, 5' ACAAC 3'  
20 3' TGTGTTGAG 5',

if StuI was employed previously to cleave the a-factor leader;

or

(2) a HgaI-HgaI adaptor, 5' AAGAAGGACAAC 3'  
25 3' CCTGTTGTTGAG 5',

if HgaI was used; and

(3) a HgaI-SalI adaptor, 5' TGAGATGATAAG 3'  
3' ACTATTCAGCT 5',

30 Cleavage of either of these ligation mixtures with BamHI and SalI yields an 870bp fragment which is isolated and ligated into pC1/1 digested to completion with the restriction enzymes BamHI and SalI and treated with alkaline phosphatase. This mixture is used to  
35 transform E. coli HB101 cells. Transformants are selected by ampicillin resistance and their plasmids analyzed by restriction endonuclease digestion.

Plasmid DNA from one selected clone (pYaEGF1) is prepared and used to transform yeast AB102 cells. Transformants are selected by their Leu<sup>+</sup> phenotype.

Assay and Characterization of Expression Product

5                    Fifty milliliter cultures of yeast strain AB102 (a, pep 4-3, leu 2-3, leu 2-112, ura 3-52, his 4-580) transformed with the above plasmid pYaEGF1 are grown at 30° in medium lacking leucine to saturation (optical density of 600nm of 5). Cell supernatants are  
10 collected by centrifugation and analyzed for the presence of human EGF using the fibroblast receptor competition binding assay. The assay of EGF is based on the ability of both mouse and human EGF to compete with <sup>125</sup>I-labeled mouse EGF for binding sites on human  
15 foreskin fibroblasts. Standard curves can be obtained by measuring the effects of increasing quantities of EGF on the binding of a standard amount of <sup>125</sup>I-labeled mouse EGF. Under these conditions 2 to 20ng of the EGF are readily measurable. Details on the binding of  
20 <sup>125</sup>I-labeled epidermal growth factor to human fibroblasts have been described by Carpenter et al., J. Biol. Chem. (1975) 250:4297. Using this assay it is found that the culture medium contains readily measurable quantities of human EGF per liter. The human EGF  
25 present in the supernatant, may be subjected to appropriate biochemical analytical methods, e.g. gel electrophoresis, HPLC and amino acid sequence analysis. The results of these procedures further confirm the identity of the product.

30                    For further characterization, human EGF present in the supernatant is purified by absorption to the ion-exchange resin Biorex-70 and elution with HCl 10mM in 80% ethanol. After evaporation of the HCl and ethanol the EGF is solubilized in water. This material  
35 migrates as a single major protein of MW approx. 6,000 in 17.5% SDS gels, roughly the same as authentic mouse EGF (MW~6,000). This indicates that the a-factor

leader sequence has been properly excised during the secretion process. Analysis by high resolution liquid chromatography (microbondapack C18, Waters column) indicates that the product migrates with a retention  
5 time similar to an authentic mouse EGF standard.

In accordance with the subject invention, novel constructs are provided which may be inserted into vectors to provide for expression of polypeptides having an N-terminal leader sequence and one or more  
10 processing signals to provide for secretion of the polypeptide as well as processing to result in a processed polypeptide product, either mature or capable of being freed of superfluous amino acids. Thus, one may obtain secretion of the pro-polypeptide which then  
15 may be subsequently processed in vivo or in vitro to provide for the mature product. In this manner, one can obtain a polypeptide having the identical amino acid sequence to a naturally occurring polypeptide. In addition, because the polypeptide can be produced in  
20 yeast, glycosylation can occur, so that a product can be obtained which is identical to or substantially identical to the naturally occurring product. Furthermore, because the product is secreted, greatly enhanced yields can be obtained based on cell population and  
25 processing and purification are greatly simplified.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be obvious that certain changes and modifications  
30 may be practiced within the scope of the appended claims.

## WHAT IS CLAIMED IS:

1. A DNA construct comprising the yeast leader sequence of a-factor including processing signals and a heterologous gene in reading frame with  
 5 said leader sequence and processing signals.

2. A DNA construct according to Claim 1 of the formula:

$$L-(PS-(\underline{a}\text{-factor}))_n\text{-PS-gene}$$

10 wherein:

L is the a-factor secretory leader sequence;  
 PS is the processing signal;  
 gene is a gene heterologous to yeast; and  
 n is 0 or 1.

15

3. A DNA construct according to Claim 2, wherein said gene is a mammalian gene or portion thereof.

20

4. A DNA construct according to Claim 2, wherein said gene is a mammalian pathogen gene or portion thereof.

5. A DNA construct of the formula:

25  $P-L-(PS-(\underline{a}\text{-factor}))_n-(PS-(\text{gene}))_r\text{-}|\text{RepS}|_q$

wherein:

P is a promoter recognized by yeast RNA polymerase;

L is the a-factor secretory leader sequence;  
 30 PS is the processing signal;  
 gene is a DNA sequence having an open reading frame in phase with L and PS encoding for a polypeptide heterologous to yeast;

q and w are at least one;

35  $|\text{RepS}|$  is a replication system recognized by yeast and may be located anywhere in the construct

external to the immediate expression region defined by P and gene as extremities; and

n and r are 0 or 1, at least one of n or r being 1.

5

6. A construct according to Claim 5, wherein r is 1 and said polypeptide is a mammalian polypeptide.

7. A construct according to Claim 5, wherein  
10 r is 1 and said polypeptide is a mammalian pathogen gene or portion thereof.

8. A construct according to Claim 5, wherein said promoter is a-factor promoter.

15

9. A construct according to Claim 5 wherein said replication system recognized by yeast is the yeast 2 $\mu$ m plasmid or portion thereof.

20 10. A construct according to Claim 5 wherein q is 2 and further comprising a replication system recognized by bacteria.

11. A method for producing a secreted  
25 polypeptide product which comprises:  
growing yeast cells containing a DNA construct according to Claim 5, whereby said secretory leader sequence, processing signals and gene encoding for said polypeptide are expressed as a fused polypeptide, which  
30 is secreted and processed by said yeast cells.

12. A method for joining two DNA fragments from diverse sources having open reading frames to be in phase, with the two fragments being first and second  
35 fragments, with at least a part of said first fragment to be an upstream fragment and at least a part of said



second fragment a downstream fragment, said method comprising:

modifying said first fragment to provide a 3'-terminus having at least two bases but not more than two bases less than a recognition site of an endonuclease;

joining to said modified 3'-terminus a linker having a 5'-terminus which completes said recognition site;

cleaving at said endonuclease recognition site; and joining said upstream and downstream fragments in reading phase by means of an adaptor.

13. A method for joining two DNA fragments from diverse sources having open reading frames to be in phase, with the two fragments being first and second fragments, with at least a part of said first fragment to be an upstream fragment and at least a part of said second fragment a downstream fragment, said method comprising:

modifying said first fragment to provide a 3'-terminus having at least two bases but not more than two bases less than a recognition site of an endonuclease;

joining to said modified 3'-terminus a linker having a 5'-terminus which completes said recognition site and defines a second endonuclease recognition site, where cleavage is directed to a site away and upstream from said recognition site;

cleaving at said second endonuclease recognition site; and joining said upstream and downstream fragments in reading phase by means of an adaptor.

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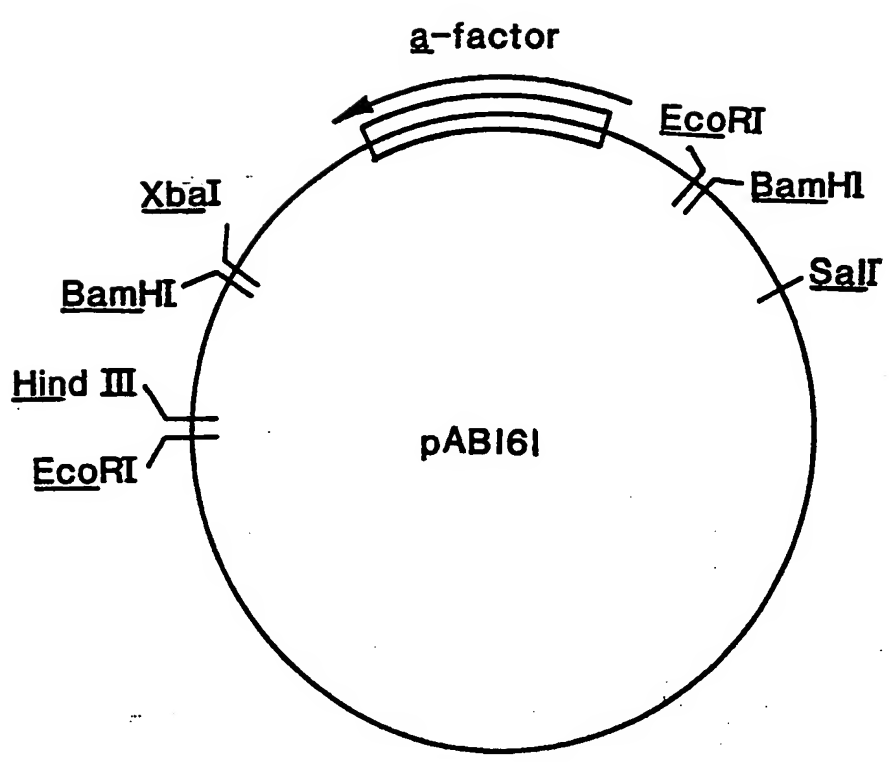


FIG. I